tics

vise Comparison of Sequences

-424-686f-10.res made by tport on Tue 20 Apr 104 13:41:22-PDT.

ng compared:US-09-424-686F-10 (1-3824)
s searched: 74
bove cutoff: 74

he initial comparison of US-09-424-686F-10 (1-3824) with:
3809.seq

Sequence Name   Description   Length Init. Score Opt. Score S

                 **** 7 standard deviations above mean ****
1. US-08-851-843A-2 Sequence 224, Application   4015   2532   3716

some SEQ ID as in 6, 26

1. US-09-424-686F-10 (1-3824)
   US-08-851-843A-2 Sequence 224, Application US/08851843A

Initial Score   = 2532   Optimized Score   = 3716   Significance =
Residue Identity   = 94%   Matches   = 3797   Mismatches   =
Gaps   = 218   Conservative Substitutions =

GTTTCAGGCAGCGGCTGCGTCCTGCTCGCGCACGTGGGAAGCCCTGGCCCGGCCCACCCCCGGCGATGC
GCAGCGCGTGCGTCCTGCTCGCGCACGTGGGAAGCCCTGGCCCGGCCCACCCCCGGCGATGC   6
      X   10   20   30   40   50   60

CTCCCCGCTGCCGAGCCGTGGCCTCCTGCTCGCGCACTACCCGCGAGGTGCTGCCGCTGGCCA   1
CTCCCCGCTGCCGAGCCGTGGCCTCCTGCTCGCGCACTACCCGCGAGGTGCTGCCGCTGGCCA   130
              80   90   100   110   120   130
        70

TGCGGGCCCTGGGGCCCCAGGGCTGCGGCTGGTGTCAGCGGGGGACCCGGCGGCTTTCCGCGCGC   210
TGCGGGCCCTGGGGCCCCAGGGCTGCGGCTGGTGTCAGCGGGGGACCCGGCGGCTTTCCGCGCGC   200
              170   180   190   200
      150   160

CCCAGTGCCTGGTGTGCGTGTCCTGGACGACGCGGCCGCCCCCGCGCCCCCTCCTTCCGCCAGG
CCCAGTGCCTGGTGTGCGTGTCCTGGACGACGCGGCCGCCCCCGCGCCCCCTCCTTCCGCCAGG   280
              240   250   260   270
      230

GCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCGTGTGCGAGCCGCGGCCCGAGAACGTGCTGG   350
GCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCGTGTGCGAGCCGCGGCCCGAGAACGTGCTGG   340
      290   300   310   320   330   340

GCTTCCGCTGCTGGACGGGGGCCCCCGGGGCCCCCCGAGGCCTTCACCCACCAGCGTGCCGCAGCT
GCTTCCGCTGCTGGACGGGGGCCCCCGGGGCCCCCCGAGGCCTTCACCCACCAGCGTGCCGCAGCT   42
      360   370   380   390   400   410

CCAACACGGTGACCGACGCACTGCGGGGGAGAGCCGGGGGGCGTGGGGCGTGCTGCTGCGCCGGTGGGCG
CCAACACGGTGACCGACGCACTGCGGGGGAGAGCCGGGGGGCGTGGGGCGTGCTGCTGCGCCGGTGGGCG   490
      430   440   450   460   470   480

TGCTGGTTCACCTGCGGCACGCTGCGCGCTGCGGCGGTCCCAGCTGCGCCTACCAGG
TGCTGGTTCACCTGCGGCACGCTGCGCGCTGCGGCGGTCCCAGCTGCGCCTACCAGG   570
      510   520   530   540   550   560

GGCCGCCGCGTGTACCAGCTCGGACGCTGCCACTCAGGCCCGGCCCCGCCCACGCTAGTGGACCCC
GGCCGCCGCGTGTACCAGCTCGGACGCTGCCACTCAGGCCCGGCCCCGCCCACGCTAGTGGACCCC   640
      580   590   600   610   620   630

GTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCCAG
GTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCCAG   710
      650   660   670   680   690   700

844   1125   1407   1688   1969   2251   2532
  3   4   5   6   7   8

PARAMETERS

Unitary   1   K-tuple   4
               5.00   Joining penalty 30
               0.33   Window size   500
               1
               0

SEARCH STATISTICS

Mean   Median   Standard Deviation
  68   14   315.92

CPU   Total Elapsed
00:00:00.01   00:00:00.00

s searched: 31716   74
bove cutoff: 74

re sorted by initial score.
lculated based on initial score.

equence to the query sequence was not found.

cores is:

13:42:29 2004

us-09-424-686f-10.res

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||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GACACCGTGTCACCTACGTCCCACTTCCTGGGGTCACTCAGGACAGCGCCAGACGCAGCTGAGTCGG
      3310        3320        3330        3340        3350        3360        3370
CGGGGACGACGCTGACTGCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACC
      3170        3180        3190        3200        3210        3220        3230
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGGGGACGACGCTGACTGCCTGGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACC
      3380        3390        3400        3410        3420        3430        3440

ACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCGAGCACCAGCAGCCCTGTCACGCCGGGGCTC
      3250        3260        3270        3280        3290        3300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCGAGCACCAGCAGCCCTGTCACGCCGGGGCTC
3450        3460        3470        3480        3490        3500        3510

CAGGGAGGGAGGGGCGGCCCACACCCAGCCGTCTGGGAGTCTGAGGCTGGAGGCCTGAGTGAGTGT
      3320        3330        3340        3350        3360        3370
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGGGAGGGAGGGGCGGCCCACACCCAGCCGTCTGGGAGTCTGAGGCTGGAGGCCTGAGTGAGTGT
      3530        3540        3550        3560        3570        3580

AGGCCTGCATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGTGTCCGGCTGAGTGTCCAGCCAAGGG
      3390        3400        3410        3420        3430        3440        3
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGGCCTGCATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGTGTCCGGCTGAGTGTCCAGCCAAGGG
      3590        3600        3610        3620        3630        3640        3650

TCCAGCACACCTGCCGTCTTCACTTCCCCACAGCTGGCGCTCCACCCAGGGCGGCCCAGCTT
      3460        3470        3480        3490        3500        3510
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCAGCACACCTGCCGTCTTCACTTCCCCACAGCTGGCGCTCGGCTCCACCCAGGGCGGCCCAGCTC
3670        3680        3690        3700        3710        3720        3730

CCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGGCATTGTTCACCC
      3540        3550        3560        3570        3580        3590
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCAGGAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGGCATTGTTCACCC
3740        3750        3760        3770        3780        3790        3800

TGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGAGAAGGACCCTGAGAAGGACCCTGGGAGCTCT
      3610        3620        3630        3640        3650        3660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGAGAAGGACCCTGAGAAGGACCCTGGGAGCTCT
3810        3820        3830        3840        3850        3860        3870

TGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGGAGACCCTGCACCTGGATGGGGGTCCCTGTGC
      3690        3700        3710        3720        3730
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGGAGACCCTGCACCTGGATGGGGGTCCCTGTGC
      3890        3900        3910        3920        3930        3940

TTTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAT
      3750        3760        3770        3780        3790        3800    X   3
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  X
TTTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAA
      3960        3970        3980        3990        4000        4010    X

3820
AAAAAAAAAA
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GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCA
      2460        2470        2480        2490        2500        2510
2320        2330        2340        2350        2360        2370
TACTTCCAGTGCCAGGGGATCCCGGCAGGGGCTCCATCCTCTTCCACGCTGCTCTGCAGCC
        |||||||||||||||||||||||||||||||||||||||||||||||||
TACTTCCAGTGCCAGGGGATCCCGGCAGGGGCTCCATCCTCTTCCACGCTGCTCTGCAGCC
530        2540        2550        2560        2570        2580

ATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTCGGTTTGGTGG
      2400        2410        2420        2430        2440
        ||||||||||||||||||||||||||||||||||||||||||||||||
ATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTCGGTTTGGTGG
0        2610        2620        2630        2640        2650

GTGACACCCTCACCCACGCGAAAAACCTTCCTCAGGACCCTGGTCACGGAGGTGTCC
      2470        2480        2490        2500        2510
        |||||||||||||||||||||||||||||||||||||||||||||||
GTGACACCCTCACCCACGCGAAAAACCTTCCTCAGGACCCTGGTCACGGAGGTGTCC
      2680        2690        2700        2710        2720

GTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCGTGTAGAAGACGGGCCCTGGGTG
      2540        2550        2560        2570        2580        2590
        |||||||||||||||||||||||||||||||||||||||||||||||||
GTGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCGTGTAGAAGACGAGCCCTGGGTG
      2750        2760        2770        2780        2790        2800

CAGATGCCGGCCTATTCCCCTGTGCGGCCTGCTGCTGGATACCCGGACCC
      2610        2620        2630        2640        2650        2660
        |||||||||||||||||||||||||||||||||||||||||||||||
CAGATGCCGGCCTATTCCCCTGTGCGGCCTGCTGCTGGATACCCGGACCC
      2820        2830        2840        2850        2860        2870

GACTACTTCCAGTC TATGCCGGACCTCCATCAGAGCCAGTCTCAACCGCGGCT
      2680        2690        2700        2710        2720        2730
        ||||||||||||||||||||||||||||||||||||||||||||||
GACTACTTCCAGTCTATGCCGGACCTCCATCAGAGCCAGTCTCAACCGCGGCT
890        2900        2910        2920        2930        2940

AACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGG
50        2760        2770        2780        2790        2800
        |||||||||||||||||||||||||||||||||||||||||||||||
AACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGG
0        2970        2980        2990        3000        3010

AGCCTCCAGACGGTGTGCACCAACATCTACAACAGATCCTCCTGCTGCGCAGGCGTACAGGT
      2830        2840        2850        2860        2870
        |||||||||||||||||||||||||||||||||||||||||||||||||
AGCCTCCAGACGGTGTGCACCAACATCTACAACAGATCCTCCTGCTGCGCAGGCGTACAGGT
      3040        3050        3060        3070        3080

CTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAACCCCACACATTTTTCCTGCGCGTCA
      2900        2910        2920        2930        2940        2950
        ||||||||||||||||||||||||||||||||||||||||||||||||
CTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAACCCCACACATTTTTCCTGCGCGTCA
      3110        3120        3130        3140        3150        3160

TCCCTCTGCTACTCCATCCTGAAAGCGCAGGATGCGCTGGGCGCCAAGG
      2970        2980        2990        3000        3010        3020
        |||||||||||||||||||||||||||||||||||||||||||||
TCCCTCTGCTACTCCATCCTGAAAGCGCAGGATGCGCTGGGCGCCAAGG
      3180        3190        3200        3210        3220        3230

CTGCCCCCGAGGCCGTGCAGTGGCCTGTGCCACCAAGCATTCTGCTCAAGCTGACTC
      3040        3050        3060        3070        3080        3090
        ||||||||||||||||||||||||||||||||||||||||||||||
CTGCCCCCGAGGCCGTGCAGTGGCCTGTGCCACCAAGCATTCTGCTCAAGCTGACTC
250        3260        3270        3280        3290        3300

TACGTGCCACTCCTGGGGTCACTCAGGACAGCAGCCCAGACGCAGCTGAGTCGGAAGCTCC
10        3120        3130        3140        3150        3160
```

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ise Comparison of Sequences

424-686f-10.res made by tport on Tue 20 Apr 104 13:41:22-PDT.

g compared:US-09-424-686F-10 (1-3824)
searched: 74
ove cutoff: 74

e initial comparison of US-09-424-686F-10 (1-3824) with:
809.seq

```
            *
       *
 |   1125 | | 1407 | |1688 | |1969 | |2251 |  2532
844|      |     |       |      |      |      |    8
63  3     4     5        6      7
2
```

PARAMETERS

Unitary	K-tuple	4
1	Joining penalty	30
5.00	Window size	500
0.33		
1		
0		

SEARCH STATISTICS

Mean	Median	Standard Deviation
68	14	315.92

CPU	Total Elapsed
00:00:00.01	00:00:00.00

searched: 31716
ove cutoff: 74
                  74

e sorted by initial score.
culated based on initial score.

equence to the query sequence was not found.

ores is:

**** 7 standard deviations above mean ****
1. US-08-851-843A-2 Sequence 224, Application 4015 2532 3716

1. US-09-424-686F-10 (1-3824)
   US-08-851-843A-2 Sequence 224, Application US/08851843A

Initial Score =	2532	Optimized Score = 3716 Significance =
Residue Identity =	94%	Matches = 3797 Mismatches =
Gaps =	218	Conservative Substitutions =

```
              10        20        30        40        50        60
GTTTCAGGCAGCGCTGCTCCTGCTGCCACGTGGGAAGCCCTGGCCCGGCCACCCCGGATGC
            |||||||||||||||||||||||||||||||||||||||||||||||
       GCAGCGGCTGCGCCTGCTGCCACGTGGGAAGCCCTGGCCCGGCCACCCCGGATGC
       X       10        20        30        40        50        61

              80        90       100       110       120       130      1
CTCCCCGCTGCCGAGCCGTGCGGCTCCCTGCTGCGCGGCCACTACCGCGAGGTGCTGCCGCTGGGCCA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CTCCCCGCTGCCGAGCCGTGCGGCTCCCTGCTGCGCGGCCACTACCGCGAGGTGCTGCCGCTGGGCCA
       70        80        90       100       110       120       130

             150       160       170       180       190       200       210
TGCGGCGCCTGGGCGCCCCAGGGCTGGCTGGCGCGGCGGGGACCCGGGACGCGGGCTTTCCGGCGGGC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCGGCGCCTGGGCGCCCCAGGGCTGGCTGGCGCGGCGGGGACCCGGGACGCGGGCTTTCCGGCGGGC
    140       150       160       170       180       190       200

             220       230       240       250       260       270       280
CCCAGTGCCCTGGTGTGCGTGCCCTGGACGCACGGCACGGCCCCCGCGCCCCGCCCCTTCCGCCAGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCCAGTGCCCTGGTGTGCGTGCCCTGGACGCACGGCACGGCCCCCGCGCCCCGCCCCTTCCGCCAGG
210       220       230       240       250       260       270

             290       300       310       320       330       340       350
GCCTGAAGGAGCTGGTGCCCGAGTGCTGCAGAGGCTGTGCGAGCGGCGGGGGAAGAACGTGCTGGI
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCTGAAGGAGCTGGTGCCCGAGTGCTGCAGAGGCTGTGCGAGCGGCGGGGGAAGAACGTGCTGGI
    290       300       310       320       330       340

             370       380       390       400       410       420
GCTTCGCGCTGCTGGACGGGGGCCCGGGGGGCCCCCCCGGAGGCTTCACCACCAGCGTGCGCAGCTI
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCTTCGCGCTGCTGGACGGGGGCCCGGGGGGCCCCCCCGGAGGCTTCACCACCAGCGTGCGCAGCTI
    360       370       380       390       400       410       420

             440       450       460       470       480       490
CCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGTGGGGGCGTGCTGCGCCGGCGCGGGGCGI
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCAACACGGTGACCGACGCACTGCGGGGAGCGGGGCGTGTGGGGGCGTGCTGCGCCGGCGCGGGGCGI
    430       440       450       460       470       480       490

             510       520       530       540       550       560       570
TGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGCTCCCAGCTGCGCCTACCAGGI
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGCTCCCAGCTGCGCCTACCAGGI
    500       510       520       530       540       550       560

             580       590       600       610       620       630       640
GGCCGGCCGTGTACCAGCTCGGCGGCTGCCACTCAGGCCCACTCAGCCCCGCCACACGGCTAGTGGACCCCI
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GGCCGCCCGCTGTACCAGCTCGGCGGCTGCCACTCAGGCCCACTCAGCCCCGCCACACGGCTAGTGGACCCCI
570       580       590       600       610       620       630

             650       660       670       680       690       700       710
GTCTGGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCCAGI
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GTCTGGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCTGGGCCTGCCAGI
650       660       670       680       690       700
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                                                                                                              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                                                                                                              GACACCGTGTCACTCTACGTGCCACTCCTGGGGTCACTCCAGGACGCAGCAGCCCCAGACGCAGCTGAGTCGGAA
                                                                                                              3310      3320      3330      3340      3350      3360      3370

3170      3180      3190      3200      3210      3220      3230
CGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCGGCACTCCCTGCCCTGCCCTCAGACTTCAAGACCAT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCGGCACTCCCTGCCCTGCCCTCAGACTTCAAGACCAT
3380      3390      3400      3410      3420      3430      3440

3240      3250      3260      3270      3280      3290      3300
ACTGATGGCCACCGCCCACACAGCCAGGCCGCAGAGCAGCACCAGCAGCCCTGTCACGCCGGGGCTCTA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTGATGGCCACCGCCCACACAGCCAGGCCGCAGAGCAGCACCAGCAGCCCTGTCACGCCGGGGCTCTA
3450      3460      3470      3480      3490      3500      3510

                                                                                                   3
CAGGGAGGGAGGGGGCGGCCCACACCCAGGCCCGCACCGGCCCGCACCACCAGGCCTGAGGCCTGAGTGAGTGTTT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CAGGGAGGGAGGGGGCGGCCCACACCCAGGCCCGCACCGGCCCGCACCACCAGGCCTGAGGCCTGAGTGAGTGTTT   35
3320      3330      3340      3350      3360      3370      3380

3390      3400      3410      3420      3430      3440      345
AGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGCGCGTGAGGCGAGTGTCCAGCCAAGGGCT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGCGCGTGAGGCGAGTGTCCAGCCAAGGGCT
3600      3610      3620      3630      3640      3650      3660

3460      3470      3480      3490      3500      3510      3520
TCCAGCACACTTGCCGTCTTCACTTCCCACAGGCTCGGCGTCTCCACCCCAGGGGCCAGCTTTT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TCCAGCACACTTGCCGTCTTCACTTCCCACAGGCTCGGCGTCTCCACCCCAGGGGCCAGCTTTT
3670      3680      3690      3700      3710      3720      3730

3530      3540      3550      3560      3570      3580      3590
CCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCT
3740      3750      3760      3770      3780      3790      3800

3600      3610      3620      3630      3640      3650      3660
TGCCCTCCTTTGCCTTCCACCCCCACCCCACCCCAGGTGGAGAACCCTGGAGAAGGACCCTGGGAGCTTCTGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCCCTCCTTTGCCTTCCACCCCCACCCCACCCCAGGTGGAGAACCCTGGAGAAGGACCCTGGGAGCTTCTGC
3810      3820      3830      3840      3850      3860      3870

                                                                                           3
TGGAGTGACCAAAGGTGTGCCCTGTACACAGCGCGAGCACCCTGCACCTGGATGGGGGTCCCCTGTGGC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGGAGTGACCAAAGGTGTGCCCTGTACACAGCGGAGCACCCTGCACCTGGATGGGGGTCCCCTGTGGC    35
3880      3890      3900      3910      3920      3930      3940

                                                                  X    381
TTGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAAA
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TTGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA    X
3950      3960      3970      3980      3990      4000      4010

3820
AAAAAAAAAA
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                                                                                              CAGCAGTGGGCCTCTTCGAGGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCA
                                                                                              2460      2470      2480      2490      2500      2510

320       2330      2340      2350      2360      2370
ACGTCCAGTGCCAGGGGATCCCGCAGGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACGTCCAGTGCCAGGGGATCCCGCAGGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC
30        2540      2550      2560      2570      2580

        2400      2410      2420      2430      2440
TGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACCGGCTGCTCCTGCGTTTGGTGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACCGGCTGCTCCTGCGTTTGGTGG
        2610      2620      2630      2640      2650

        2470      2480      2490      2500      2510
TGACACCTCACCTCACCCACGGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGACACCTCACCTCACCCACGGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCC
2680      2690      2700      2710      2720

        2540      2550      2560      2570      2580      2590
TGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTG
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGGTGAACTTGCGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTG
2750      2760      2770      2780      2790      2800

        2610      2620      2630      2640      2650      2660
AGATGGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCCTGCTGCTGGATACCCGGACCC
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AGATGGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCCTGCTGCTGGATACCCGGACCC
2820      2830      2840      2850      2860      2870

680       2690      2700      2710      2720      2730
ACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCCAGTCTCACCTTCAACCGCGGCT
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCCAGTCTCACCTTCAACCGCGGCT
90        2900      2910      2920      2930      2940

0         2760      2770      2780      2790      2800
ACATGCGTCGCAAACTCTTTGGGGTCTTGCGCGGCTGAAGTGTCACAGCCTGTTTCTGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ACATGCGTCGCAAACTCTTTGGGGTCTTGCGCGGCTGAAGTGTCACAGCCTGTTTCTGG
2970      2980      2990      3000      3010

        2830      2840      2850      2860      2870
GCCTCCAGACGCGTGTGCACCAACATCTACAAGATCCTTCCTGCTCGCTGCCGGCGTACAGGT
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
GCCTCCAGACGCGTGTGCACCAACATCTACAAGATCCTTCCTGCTCGCTGCCGGCGTACAGGT
3040      3050      3060      3070      3080

        2900      2910      2920      2930      2940      2950
TGCAGCTCCCCATTTCATCAGCAAGTTTGGAAGAACCCCACCATTTTCTGCGCCGTCA
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCAGCTCCCCATTTCATCAGCAAGTTTGGAAGAACCCCACCATTTTCTGCGCCGTCA
3110      3120      3130      3140      3150      3160

2970      2980      2990      3000      3010      3020
CCCTCTGCTGTACTCCATCCTGAAAGCCGAGAACGCGAGGATGTCGCTGGGGGCCAAGG
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
CCCTCTGCTGTACTCCATCCTGAAAGCCGAGAACGCGAGGATGTCGCTGGGGGCCAAGG
3180      3190      3200      3210      3220      3230

040       3050      3060      3070      3080      3090
TGCCCTCCGAGGCCGTGCAGTGGCCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TGCCCTCCGAGGCCGTGCAGTGGCCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
50        3260      3270      3280      3290      3300

0         3120      3130      3140      3150      3160
ACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGGCGCAGCTGAGTCGGAAGCTCC
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